

## SEQUENCE LISTING

&lt;110&gt; OTSUKA PHARMACEUTICAL CO., LTD.

&lt;120&gt; LY6H GENE

&lt;130&gt; Q63396

&lt;150&gt; JP 1998-263550

&lt;151&gt; 1998-09-17

&lt;160&gt; 3

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; human embryonic brain

&lt;400&gt; 1

Met Leu Pro Ala Ala Met Lys Gly Leu Gly Leu Ala Leu Leu Ala Val  
1 5 10 15

Leu Leu Cys Ser Ala Pro Ala His Gly Leu Trp Cys Gln Asp Cys Thr  
20 25 30

Leu Thr Thr Asn Ser Ser His Cys Thr Pro Lys Gln Cys Gln Pro Ser  
35 40 45

Asp Thr Val Cys Ala Ser Val Arg Ile Thr Asp Pro Ser Ser Ser Arg  
50 55 60

Lys Asp His Ser Val Asn Lys Met Cys Ala Ser Ser Cys Asp Phe Val  
65 70 75 80

Lys Arg His Phe Phe Ser Asp Tyr Leu Met Gly Phe Ile Asn Ser Gly  
85 90 95

Ile Leu Lys Val Asp Val Asp Cys Cys Glu Lys Asp Leu Cys Asn Gly  
100 105 110

Ala Ala Gly Ala Gly His Ser Pro Trp Ala Leu Ala Gly Gly Leu Leu  
115 120 125

Leu Ser Leu Gly Pro Ala Leu Leu Trp Ala Gly Pro  
130 135 140

&lt;210&gt; 2

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature  
<223> human embryonic brain

<400> 2  
atgctgcctg cagccatgaa gggcctcggc ctggcgctgc tggcgtcct gctgtgctcg 60  
gcgcccgcctc atggcctgtg gtgccaggac tgcaccctga ccaccaactc cagccattgc 120  
accccaaagc agtgccagcc gtccgacacg gtgtgtgcca gtgtccgaat caccgatccc 180  
agcagcagca ggaaggatca ctcggtgaac aagatgtgtg cctcctcctg tgacttcggt 240  
aagcgacact ttttctcaga ctatctgatg gggtttatta actctgggat cttaaaggtc 300  
gacgtggact gctgcgagaa ggatttgtgc aatggggcgg caggggcagg gcacagcccc 360  
tggggcctgg ccgggggggt cctgctcagc ctggggcctg ccctcctctg ggctgggccc 420

<210> 3  
<211> 854  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> human embryonic brain

<220>  
<221> exon  
<222> (99)..(518)

<400> 3  
acgccgcccc agcccggagt gcggacaccc ccgggatgct tgcgccccag aggacccgcg 60  
ccccaaagccc ccgcgccgcc cccaggccca cccggagc atg ctg cct gca gcc atg 116  
Met Leu Pro Ala Ala Met  
1 5  
aag ggc ctc ggc ctg gcg ctg ctg gcc gtc ctg ctg tgc tcg gcg ccc 164  
Lys Gly Leu Gly Leu Ala Leu Leu Ala Val Leu Leu Cys Ser Ala Pro  
10 15 20  
gct cat ggc ctg tgg tgc cag gac tgc acc ctg acc acc aac tcc agc 212  
Ala His Gly Leu Trp Cys Gln Asp Cys Thr Leu Thr Thr Asn Ser Ser  
25 30 35  
cat tgc acc cca aag cag tgc cag ccg tcc gac acg gtg tgt gcc agt 260  
His Cys Thr Pro Lys Gln Cys Gln Pro Ser Asp Thr Val Cys Ala Ser  
40 45 50  
gtc cga atc acc gat ccc agc agc agc agg aag gat cac tcg gtg aac 308  
Val Arg Ile Thr Asp Pro Ser Ser Ser Arg Lys Asp His Ser Val Asn  
55 60 65 70  
aag atg tgt gcc tcc tcc tgt gac ttc gtt aag cga cac ttt ttc tca 356  
Lys Met Cys Ala Ser Ser Cys Asp Phe Val Lys Arg His Phe Phe Ser  
75 80 85

gac tat ctg atg ggg ttt att aac tct ggg atc tta aag gtc gac gtg	404
Asp Tyr Leu Met Gly Phe Ile Asn Ser Gly Ile Leu Lys Val Asp Val	
90 95 100	
gac tgc tgc gag aag gat ttg tgc aat ggg gcg gca ggg gca ggg cac	452
Asp Cys Cys Glu Lys Asp Leu Cys Asn Gly Ala Ala Gly Ala Gly His	
105 110 115	
agc ccc tgg gcc ctg gcc ggg ggg ctc ctg ctc agc ctg ggg cct gcc	500
Ser Pro Trp Ala Leu Ala Gly Gly Leu Leu Leu Ser Leu Gly Pro Ala	
120 125 130	
ctc ctc tgg gct ggg ccc tgatgtctcc tccttcccac ggggcttctg	548
Leu Leu Trp Ala Gly Pro	
135 140	
agcttgctcc cctgagcctg tggtgtccct ctccccagcc tggcgtggct ggggctggg	608
gcagccttgg cccagctccg tggtgtggc ctgtggctct cactcctccc ccgacgtgaa	668
gcctccctgt ctctccgcca gctctgagtc ccaggcagct ggacatctcc aggaaaccag	728
gccatctggg caggaggcct ggggatgagg gtggggggggg acccccaggt cccggagggg	788
aagtgaagca acagcccagc tggaagggcg tcttctgcgg agaaataaag tcacttttga	848
gtcctg	854